

**EXHIBIT B**  
**U.S. CLAIMS**

38. (New) A set of nucleic acid segments for identifying the CCR5 haplotype group of both alleles of a human subject, wherein said set of nucleic acid segments comprises at least one nucleic acid segment capable of detecting each of the following haplotype groups, each CCR5 haplotype group (haplogroup) being defined in terms of the nucleotides at positions 29, 208, 303, 627, 630, 676 and 927 of the human CCR5 sequence of SEQ ID NO:65, with definition of the amino acid at position 64 and the presence or absence of the  $\Delta 32$  deletion of the human CCR2 sequence, as follows:

Haplogroup	Nucleotide position in CCR5 sequence						
	29	208	303	627	730	676	927
HHA:	A	G	G	T	C	A	C
HHB:	A	T	G	T	C	A	C
HHC:	A	T	G	T	C	G	C
HHD:	A	T	G	T	T	A	C
HHE:	A	G	A	C	C	A	C
HHF*1:	A	G	A	C	C	A	T
HHF*2:	A	G	A	C	C	A	T
HHG*1:	G	G	A	C	C	A	C
HHG*2:	G	G	A	C	C	A	C

isoleucine at amino acid 64

has  $\Delta 32$ , 32 base pair deletion

39. (New) The set of nucleic acid segments of claim 38, further comprising at least one nucleic acid segment capable of detecting a human CCR2 polymorphism at both alleles.

40. (New) The set of nucleic acid segments of claim 39, further comprising at least a first and a second nucleic acid segment that is each capable of detecting a distinct human CCR2 polymorphism at both alleles.

41. (New) The set of nucleic acid segments of claim 38, wherein each of said nucleic acid segments is a primer.

42. (New) A kit comprising a set of nucleic acid segments in accordance with claim 38 and a suitable container for said set of nucleic acid segments.

43. (New) The kit of claim 42, further comprising instructions for identifying the CCR5 haplotype group of both alleles of a human subject and for correlating the haplogroups on both CCR5 alleles with the risk of HIV-1 infection or disease progression in humans.

44. (New) The kit of claim 42, further comprising a restriction endonuclease.
45. (New) The kit of claim 42, further comprising at least one nucleic acid segment capable of detecting a human CCR2 polymorphism at both alleles.
46. (New) The kit of claim 42, further comprising at least a first and a second nucleic acid segment that is each capable of detecting a distinct human CCR2 polymorphism at both alleles.
47. (New) The kit of claim 42, wherein each of said nucleic acid segments is a primer.
48. (New) The kit of claim 42, further comprising at least a first anti-viral therapeutic agent.
49. (New) A method of identifying the CCR5 haplotype group of a human subject, comprising identifying the CCR5 haplotype group of both alleles of a human subject using a set of nucleic acid segments in accordance with claim 38.
50. (New) A method of identifying the CCR5 haplotype group of each member of a cohort of human subjects of a chosen population, comprising identifying the CCR5 haplotype group of both alleles of each member of said cohort of human subjects of said chosen population using a set of nucleic acid segments in accordance with claim 38 and determining the correlation of said CCR5 haplotype group of both alleles with risk of HIV-1 infection, transmission or disease progression in said population.
51. (New) The method of claim 50, wherein said population is an ethnic group.
52. (New) The method of claim 50, wherein said population is children.
53. (New) The method of claim 50, further comprising identifying the human CCR2 polymorphisms at both alleles and further correlating said CCR2 polymorphisms with risk of HIV-1 infection, transmission or disease progression in said population.

54. (New) A method of assessing the risk of a human subject for HIV-1 infection, transmission or disease progression, comprising identifying the CCR5 haplotype group of both alleles of said human subject using a set of nucleic acid segments in accordance with claim 38, and correlating the pair of haplogroups identified with the risk of HIV-1 infection, transmission or disease progression associated with said pair of haplogroups.

55. (New) The method of claim 54, wherein said pair of haplogroups identified for the human subject is correlated with the risk of HIV-1 infection, transmission or disease progression associated with that pair of haplogroups for a population to which the subject belongs.

56. (New) The method of claim 54, wherein said human subject is Caucasian and the presence of two HHE alleles is indicative of an increased risk of HIV-1 infection or disease progression.

57. (New) The method of claim 54, wherein said human subject is African-American and the presence of an HHC and an HHF\*1 haplogroup, an HHC and an HHE haplogroup, two HHC haplogroups, or an HHC and an HHD haplogroup is indicative of an increased risk of HIV-1 infection or disease progression.

58. (New) The method of claim 54, wherein said human subject is a child and the presence of an HHC and an HHE haplogroup, two HHE haplogroups, or an HHE haplogroup and an HHG\*2 haplogroup is indicative of an increased risk of HIV-1 transmission, infection or disease progression.

59. (New) The method of claim 54, wherein a human subject identified as having an increased risk of HIV-1 infection or disease progression is treated with a biologically effective amount of at least a first anti-viral agent.

60. (New) A method of reducing HIV-1 infection, transmission or disease progression in a human subject, comprising:

- (a) identifying a susceptible human subject by:
  - (i) identifying the CCR5 haplotype group of both alleles of said human subject using a set of nucleic acid segments in accordance with claim 38; and
  - (ii) correlating the pair of haplogroups identified with the risk of HIV-1 infection, transmission or disease progression associated with said pair of haplogroups; and

- (b) treating said susceptible human subject with a biologically effective amount of at least a first anti-viral agent.

61. (New) A nucleic acid segment for identifying a CCR5 haplotype group of a human subject, which nucleic acid segment is capable of detecting the human haplotype group HHD, which has nucleotide A at position 29, T at position 208, G at position 303, T at position 627, T at position 630, A at position 676 and C at position 927 of the human CCR5 sequence of SEQ ID NO:65.

62. (New) The nucleic acid segment of claim 61, comprised within a set of nucleic acid segments for identifying the CCR5 haplotype group of both alleles of a human subject.